

RAW SEQUENCE LISTING  
PATENT APPLICATION US/08/167,628DATE: 02/16/94  
TIME: 13:53:25

INPUT SET: S866.raw

## SEQUENCE LISTING

## (1) General Information:

(i) APPLICANT: Grotendorst, Gary R.  
Bradham Jr., Douglas M.,

(ii) TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR

(iii) NUMBER OF SEQUENCES: 2

## (iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Spensley Horn Jubas & Lubitz  
(B) STREET: 4225 Executive Square, Suite 1400  
(C) CITY: La Jolla  
(D) STATE: CA  
(E) COUNTRY: US  
(F) ZIP: 92037

## (v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

## (vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US/08/167,628  
(B) FILING DATE:  
(C) CLASSIFICATION:

## (vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US/07/752,427  
(B) FILING DATE:

## (viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Wetherell, Jr. Ph.D., John W.  
(B) REGISTRATION NUMBER: 31,678  
(C) REFERENCE/DOCKET NUMBER: PD-1294

## (ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 619-455-5100  
(B) TELEFAX: 619-455-5110

## (2) INFORMATION FOR SEQ ID NO:1:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2075 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

ENTERED

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 DATE: 02/16/94  
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52
53      (ii) MOLECULE TYPE: cDNA
54
55
56      (vii) IMMEDIATE SOURCE:
57            (B) CLONE: DB60R32
58
59      (ix) FEATURE:
60            (A) NAME/KEY: CDS
61            (B) LOCATION: 130..1177
62
63
64      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
65
66      CCCGGCCGAC AGCCCCGAGA CGACAGCCCG GCGCGTCCCG GTCCCCACCT CCGACCACCG      60
67
68      CCAGCGCTCC AGGCCCCGCG CTCCCCGCTC GCCGCCACCG CGCCCTCCGC TCCGCCCGCA      120
69
70      GTGCCAACC ATG ACC GCC GCC AGT ATG GGC CCC GTC CGC GTC GCC TTC      168
71            Met Thr Ala Ala Ser Met Gly Pro Val Arg Val Ala Phe
72            1              5              10
73
74      GTG GTC CTC CTC GCC CTC TGC AGC CGG CCG GCC GTC GGC CAG AAC TGC      216
75      Val Val Leu Leu Ala Leu Cys Ser Arg Pro Ala Val Gly Gln Asn Cys
76            15              20              25
77
78      AGC GGG CCG TGC CGG TGC CCG GAC GAG CCG GCG CCG CGC TGC CCG GCG      264
79      Ser Gly Pro Cys Arg Cys Pro Asp Glu Pro Ala Pro Arg Cys Pro Ala
80            30              35              40              45
81
82      GGC GTG AGC CTC GTG CTG GAC GGC TGC GGC TGC TGC CGC GTC TGC GCC      312
83      Gly Val Ser Leu Val Leu Asp Gly Cys Gly Cys Cys Arg Val Cys Ala
84            50              55              60
85
86      AAG CAG CTG GGC GAG CTG TGC ACC GAG CGC GAC CCC TGC GAC CCG CAC      360
87      Lys Gln Leu Gly Glu Leu Cys Thr Glu Arg Asp Pro Cys Asp Pro His
88            65              70              75
89
90      AAG GGC CTC TTC TGT GAC TTC GGC TCC CCG GCC AAC CGC AAG ATC GGC      408
91      Lys Gly Leu Phe Cys Asp Phe Gly Ser Pro Ala Asn Arg Lys Ile Gly
92            80              85              90
93
94      GTG TGC ACC GCC AAA GAT GGT GCT CCC TGC ATC TTC GGT GGT ACG GTG      456
95      Val Cys Thr Ala Lys Asp Gly Ala Pro Cys Ile Phe Gly Gly Thr Val
96            95              100              105
97
98      TAC CGC AGC GGA GAG TCC TTC CAG AGC AGC TGC AAG TAC CAG TGC ACG      504
99      Tyr Arg Ser Gly Glu Ser Phe Gln Ser Ser Cys Lys Tyr Gln Cys Thr
100     110              115              120              125
101
102     TGC CTG GAC GGG GCG GTG GGC TGC ATG CCC CTG TGC AGC ATG GAC GTT      552
  
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**INPUT SET: S866.raw**

103	Cys	Leu	Asp	Gly	Ala	Val	Gly	Cys	Met	Pro	Leu	Cys	Ser	Met	Asp	Val	
104					130					135					140		
105																	
106	CGT	CTG	CCC	AGC	CCT	GAC	TGC	CCC	TTC	CCG	AGG	AGG	GTC	AAG	CTG	CCC	600
107	Arg	Leu	Pro	Ser	Pro	Asp	Cys	Pro	Phe	Pro	Arg	Arg	Val	Lys	Leu	Pro	
108				145					150					155			
109																	
110	GGG	AAA	TGC	TGC	GAG	GAG	TGG	GTG	TGT	GAC	GAG	CCC	AAG	GAC	CAA	ACC	648
111	Gly	Lys	Cys	Cys	Glu	Glu	Trp	Val	Cys	Asp	Glu	Pro	Lys	Asp	Gln	Thr	
112			160					165					170				
113																	
114	GTG	GTT	GGG	CCT	GCC	CTC	GCG	GCT	TAC	CGA	CTG	GAA	GAC	ACG	TTT	GGC	696
115	Val	Val	Gly	Pro	Ala	Leu	Ala	Ala	Tyr	Arg	Leu	Glu	Asp	Thr	Phe	Gly	
116		175					180					185					
117																	
118	CCA	GAC	CCA	ACT	ATG	ATT	AGA	GCC	AAC	TGC	CTG	GTC	CAG	ACC	ACA	GAG	744
119	Pro	Asp	Pro	Thr	Met	Ile	Arg	Ala	Asn	Cys	Leu	Val	Gln	Thr	Thr	Glu	
120	190					195					200					205	
121																	
122	TGG	AGC	GCC	TGT	TCC	AAG	ACC	TGT	GGG	ATG	GGC	ATC	TCC	ACC	CGG	GTT	792
123	Trp	Ser	Ala	Cys	Ser	Lys	Thr	Cys	Gly	Met	Gly	Ile	Ser	Thr	Arg	Val	
124					210					215					220		
125																	
126	ACC	AAT	GAC	AAC	GCC	TCC	TGC	AGG	CTA	GAG	AAG	CAG	AGC	CGC	CTG	TGC	840
127	Thr	Asn	Asp	Asn	Ala	Ser	Cys	Arg	Leu	Glu	Lys	Gln	Ser	Arg	Leu	Cys	
128				225					230					235			
129																	
130	ATG	GTC	AGG	CCT	TGC	GAA	GCT	GAC	CTG	GAA	GAG	AAC	ATT	AAG	AAG	GGC	888
131	Met	Val	Arg	Pro	Cys	Glu	Ala	Asp	Leu	Glu	Glu	Asn	Ile	Lys	Lys	Gly	
132			240					245					250				
133																	
134	AAA	AAG	TGC	ATC	CGT	ACT	CCC	AAA	ATC	TCC	AAG	CCT	ATC	AAG	TTT	GAG	936
135	Lys	Lys	Cys	Ile	Arg	Thr	Pro	Lys	Ile	Ser	Lys	Pro	Ile	Lys	Phe	Glu	
136		255					260					265					
137																	
138	CTT	TCT	GGC	TGC	ACC	AGC	ATG	AAG	ACA	TAC	CGA	GCT	AAA	TTC	TGT	GGA	984
139	Leu	Ser	Gly	Cys	Thr	Ser	Met	Lys	Thr	Tyr	Arg	Ala	Lys	Phe	Cys	Gly	
140	270					275					280					285	
141																	
142	GTA	TGT	ACC	GAC	GGC	CGA	TGC	TGC	ACC	CCC	CAC	AGA	ACC	ACC	ACC	CTG	1032

RAW SEQUENCE LISTING  
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154 GAC ATC TTT GAA TCG CTG TAC TAC AGG AAG ATG TAC GGA GAC ATG GCA T 1177  
155 Asp Ile Phe Glu Ser Leu Tyr Tyr Arg Lys Met Tyr Gly Asp Met Ala  
156 335 340 345  
157  
158 GAAGCCAGAG AGTGAGAGAC ATTAAGTTCAT TAGACTGGAA CTTGAACTGA TTCACATCTC 1237  
159  
160 ATTTTCCGT AAAAATGATT TCAGTAGCAC AAGTTATTTA AATCTGTTTT TCTAACTGGG 1297  
161  
162 GGAAAAGATT CCCACCCAAT TCAAAACATT GTGCCATGTC AAACAAATAG TCTATCTTCC 1357  
163  
164 CCAGACACTG GTTTGAAGAA TGTTAAGACT TGACAGTGGA ACTACATTAG TACACAGCAC 1417  
165  
166 CAGAATGTAT ATTAAGGTGT GGCTTTAGGA GCAGTGGGAG GGTACCGGCC CGGTTAGTAT 1477  
167  
168 CATCAGATCG ACTCTTATAC GAGTAATATG CCTGCTATTT GAAGTGTAAT TGAGAAGGAA 1537  
169  
170 AATTTTAGCG TGCTCACTGA CCTGCCTGTA GCCCCAGTGA CAGCTAGGAT GTGCATTCTC 1597  
171  
172 CAGCCATCAA GAGACTGAGT CAAGTTGTTC CTTAAGTCAG AACAGCAGAC TCAGCTCTGA 1657  
173  
174 CATTCTGATT CGAATGACAC TGTTTCAGGAA TCGGAATCCT GTCGATTAGA CTGGACAGCT 1717  
175  
176 TGTGGCAAGT GAATTTGCCT GTAACAAGCC AGATTTTTTA AAATTTATAT TGTAATATT 1777  
177  
178 GTGTGTGTGT GTGTGTGTGT ATATATATAT ATATATGTAC AGTTATCTAA GTTAATTTAA 1837  
179  
180 AGTTGTTTGT GCCTTTTTAT TTTTGTTTTT AATGCTTTGA TATTTCAATG TTAGCCTCAA 1897  
181  
182 TTTCTGAACA CCATAGGTAG AATGTAAAGC TTGTCTGATC GTTCAAAGCA TGAAATGGAT 1957  
183  
184 ACTTATATGG AAATTCTGCT CAGATAGAAT GACAGTCCGT CAAAACAGAT TGTTTGCAAA 2017  
185  
186 GGGGAGGCAT CAGTGTCTTG GCAGGCTGAT TTCTAGGTAG GAAATGTGGT AGCTCACG 2075  
187  
188  
189 (2) INFORMATION FOR SEQ ID NO:2:  
190  
191 (i) SEQUENCE CHARACTERISTICS:  
192 (A) LENGTH: 349 amino acids  
193 (B) TYPE: amino acid  
194 (D) TOPOLOGY: linear  
195  
196 (ii) MOLECULE TYPE: protein  
197  
198 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:  
199  
200 Met Thr Ala Ala Ser Met Gly Pro Val Arg Val Ala Phe Val Val Leu  
201 1 5 10 15  
202  
203 Leu Ala Leu Cys Ser Arg Pro Ala Val Gly Gln Asn Cys Ser Gly Pro  
204 20 25 30

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205																
206	Cys	Arg	Cys	Pro	Asp	Glu	Pro	Ala	Pro	Arg	Cys	Pro	Ala	Gly	Val	Ser
207			35					40					45			
208																
209	Leu	Val	Leu	Asp	Gly	Cys	Gly	Cys	Cys	Arg	Val	Cys	Ala	Lys	Gln	Leu
210		50					55					60				
211																
212	Gly	Glu	Leu	Cys	Thr	Glu	Arg	Asp	Pro	Cys	Asp	Pro	His	Lys	Gly	Leu
213	65					70					75					80
214																
215	Phe	Cys	Asp	Phe	Gly	Ser	Pro	Ala	Asn	Arg	Lys	Ile	Gly	Val	Cys	Thr
216					85					90					95	
217																
218	Ala	Lys	Asp	Gly	Ala	Pro	Cys	Ile	Phe	Gly	Gly	Thr	Val	Tyr	Arg	Ser
219				100					105					110		
220																
221	Gly	Glu	Ser	Phe	Gln	Ser	Ser	Cys	Lys	Tyr	Gln	Cys	Thr	Cys	Leu	Asp
222			115					120					125			
223																
224	Gly	Ala	Val	Gly	Cys	Met	Pro	Leu	Cys	Ser	Met	Asp	Val	Arg	Leu	Pro
225		130					135					140				
226																
227	Ser	Pro	Asp	Cys	Pro	Phe	Pro	Arg	Arg	Val	Lys	Leu	Pro	Gly	Lys	Cys
228	145					150					155					160
229																
230	Cys	Glu	Glu	Trp	Val	Cys	Asp	Glu	Pro	Lys	Asp	Gln	Thr	Val	Val	Gly
231					165					170					175	
232																
233	Pro	Ala	Leu	Ala	Ala	Tyr	Arg	Leu	Glu	Asp	Thr	Phe	Gly	Pro	Asp	Pro
234				180					185					190		
235																
236	Thr	Met	Ile	Arg	Ala	Asn	Cys	Leu	Val	Gln	Thr	Thr	Glu	Trp	Ser	Ala
237			195					200					205			
238																
239	Cys	Ser	Lys	Thr	Cys	Gly	Met	Gly	Ile	Ser	Thr	Arg	Val	Thr	Asn	Asp
240		210					215					220				
241																
242	Asn	Ala	Ser	Cys	Arg	Leu	Glu	Lys	Gln	Ser	Arg	Leu	Cys	Met	Val	Arg
243	225					230					235					240
244																
245	Pro	Cys	Glu	Ala	Asp	Leu	Glu	Glu	Asn	Ile	Lys	Lys	Gly	Lys	Lys	Cys
246					245					250					255	
247																
248	Ile	Arg	Thr	Pro	Lys	Ile	Ser	Lys	Pro	Ile	Lys	Phe	Glu	Leu	Ser	Gly
249				260					265					270		
250																
251	Cys	Thr	Ser	Met	Lys	Thr	Tyr	Arg	Ala	Lys	Phe	Cys	Gly	Val	Cys	Thr
252			275					280					285			
253																
254	Asp	Gly	Arg	Cys	Cys	Thr	Pro	His	Arg	Thr	Thr	Thr	Leu	Pro	Val	Glu
255		290					295					300				

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256  
257 Phe Lys Cys Pro Asp Gly Glu Val Met Lys Lys Asn Met Met Phe Ile  
258 305 310 315 320  
259  
260 Lys Thr Cys Ala Cys His Tyr Asn Cys Pro Gly Asp Asn Asp Ile Phe  
261 325 330 335  
262  
263 Glu Ser Leu Tyr Tyr Arg Lys Met Tyr Gly Asp Met Ala  
264 340 345  
265

**SEQUENCE VERIFICATION REPORT**  
**PATENT APPLICATION US/08/167,628**

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*INPUT SET: S866.raw*

Line	Error	Original Text
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PAGE: 1

**SEQUENCE MISSING ITEM REPORT**  
**PATENT APPLICATION US/08/167,628**

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*INPUT SET: S866.raw*

< < THERE ARE NO ITEMS MISSING > >



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**SEQUENCE CORRECTION REPORT**  
**PATENT APPLICATION US/08/167,628**

DATE: 02/16/94  
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*INPUT SET: S866.raw*

Line	Original Text	Corrected Text
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